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OM protein -
                                                                                      protein search, using sw model
                                                     November 9, 2002, 04:28:16;
                                                                                                                                                 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
; Search time 49 Seconds
(without alignments)
372.766 Million cell updates/sec
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Title: Perfect score: US-09-895-298A-83 1002

Sequence: 1 MMNFQPPSKAWRASQMMTFF......HDGSLDLRSRRSVQEGNPRA 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

283224

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR\_73:\* pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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RESULT 2 A96920

probable ABC transporter, permease component CAC0165 [imported] - Clostridium acetobu | C;Species: Clostridium acetobutylicum | C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001 | C;Accession: A96920 | R;Nolling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 | A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325 | A;Accession: A96920 | A;Status: preliminary A;Molecule type: DNA

54420
76.5 76.5 75.7 75.5 75.5 75.5 74.7 74.5 74.5
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D37753 D81336 H64959 T47467 T24975 T16073 JE0084 T43731 H711896 F86764 E22845 S58883 T12787 A82997 A82997
PnuC protein - Sal probable K+ uptake probable membrane hypothetical prote hypothetical prote hypothetical prote hypothetical sodi cell wall alpha gl hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote calcium-channel ho probable protein-d hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote

## ALIGNMENTS

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113 RKIMIRLLHEQIINEGKDKMF 133 : :    :   :   :         :  807 QDLSFQLMVERTEEKKKIF 825	64 SWIDTLSTRPGYLWVWIYRNLIGSVHFFFILTLIVLIITYLYWQITEG 112 :     ; ;   ; ; ; ;   ;   ;   ;   ;   ;	6 PPSKAWRASQMMTFFIFLLFFPSFTGVLCTLAITIWRLKPSADCGPFRGLPLFIHSIY 63    : :   :	Query Match 9.9%; Score 99.5; DB 2; Length 1203; Best Local Similarity 27.7%; Pred. No. 0.45; Matches 39; Conservative 23; Mismatches 50; Indels 29; Gaps 8;	A;Molecule type: DNA A;Residues: 1-1203 <sto> A;Residues: 1-203 <sto> A;Cross-references: GB:chr_X; PIDN:AAB36841.2; PID:g4850180; GSPDB:GN00028; CESP:B041   C;Genetics: A;Gene: B0416.1 A;Map position: X</sto></sto>	A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio   A;Reference number: A75000; MUID:99069613; PMID:9851916 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: H89606 A;Status: preliminary	RESULT 1  H89606  H89606  protein B0416.1 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001 C;Accession: H89606 R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998

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C;Opecies: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Caccession: C70905
C;Accession: C70905
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70905
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-322 <COL>
A;Cross-references: GB:Z97050; GB:AL123456; NID:g3256008; PIDN:CAB09743.1; PID:g2213513
A;Cross-references: Strain H37Rv
C;Genetics:
A;Gene: Rv0176
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv0176
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A;Cross-references: GB:AE001437; PIDN:AAK78148.1; PID:g15022994; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0165
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                                                                                                                                                                        hypothetical protein C56A3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20264
                                                               R:Sims, M.
submitted to the EMBL Data Library
A; Reference number: Z19244
A; Accession: T20264
A; Status: preliminary; translated
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                     A; Mclecule type: DNA
A; Residues: 1-261 <WIL>
A; Cross-references: EMBL: Z77655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPSKAWR--ASQMMTFFIFL-----LFFPSFTGVLCTLAITIWRL--KPSADCGPFRGLP 56
                                                                                                                                                                                                                                                                                                                                                                                           LFIHSIYSWIDTLSTRPGYLWVVW
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26; Conserv
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                                                                                                                                      Library, July 1996
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 88; DB 2
Pred. No. 1.2;
14; Mismatches
         PIDN:CAB01133.1;
                                                                          from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                            132
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             GSPDB:GN00023; CESP:C56A3.4
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A;Experimental source: clone C56A3 C;Genetics:
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A; Introns: 107/3; 135/2;
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A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: H85355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: AT4930430
A;Map position: 4
C;Superfamily: Arabidopsis thaliana hypothetical protein F9K21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; anonymous, The European Union Arabidopsis Genome Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                 hypothetical protein BH0280 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C; Decies: Bacillus halodurans C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C; Date: 01-Dec-2000 Ftext_change 15-Jun-2001 C; Da
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A; Residues: 1-272 <STO>
A; Cross-references: GB:
C; Genetics:
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A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB03999.1; GSPDB:GA;Experimental source: strain C-125 C;Genetics:
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                                                                                                A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-713 <STO>
                                                                                                                                                                                              R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeuo, G.; Sasaki, N.; Nucleic Acids Res. 28, 4317-4331, 2000

A; Title: Complete genome sequence of the alkaliphilic bacterium A; Reference number: A83650; MUID:20512582; PMID:11058132

A; Accession: H83684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----YLWVVWIYRNLIGSVHFFFILTLIVLIITYLYWQIT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILNFFVFLLSVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 27; Conserv
                                                                                                                                                                                                                                                                                              Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.;
Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:NC_001268; NID:g7269944;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.7%;
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Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 87; DB Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                    Masui, N.; Fuji,
                                                                                                                                                                                                                                                                                           Bacillus
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: D70072
R;Kunst, F:; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
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Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Accession: D70072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16029.1; PID:e1184718.
A;Experimental source: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 PKTLAWTLWGITGLMLMFYIMRNGKTVAIYSMHGFSLF-------KIWRRLIGN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 TYLYWQITEGRKIMIRLLHEQIINEGKDKMFLIEK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                           54 GLPLFIHSIYSWIDTL----
                                                                                                                                                                                                                                                                                                                                                                  4 FQPPSKAW-----RASQMMTFFIFLL---FFPSF-TGVLCTLAITIWRLKPSADCGPFR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 PPSKAWR----ASQMMTFFI-------FLLFFPSFTGVLCTLAITIWRLKPSA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DCGPFRG-----LPLFIHSIYSWIDTLSTRPGYLWVVWIYRNLIGSVHFFFILTLIVLII 102
                                                                                                      -FPFLLVMVIYLLLFIW---
                                                                                                                                                    HFFFILTLIVLIITYLYWQITEGRKIMIRLLHEQIINEG----KDKMFLIEKLIKL 141
                                                                                                                                                                                                                                                                                                             FEVPSGVFADRYGIKISIASSFFFSILTWAFFPFIDSAAICILAMIIWALSDSLISGSFE 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type: DNA
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                                                                                                                                                                                                      -TWMSRVAGEDRFGKEMMKNTQLLITFLIIGSIASGYLYSLNIY------
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                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 3.6; 31; Mismatches
                                                                                                    --MSVFIKVPSVSETNHGDQNQHDSIKIIKESLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 84;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 84.5; D
Pred. No. 6.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                         ----STRPGYLWVVWIYRNLIGSV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 399;
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89;
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A;Cross-references: GB:AL592022; PIDN:CAC97188.1; PID:g16414459; GSPDB:GN00178 A;Experimental source: strain Clip11262 C;Genetics:
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AD1677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: AH2288
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C;Superfamily: lipoprotein signal peptidase
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A; Residues: 1-154 <GLA>
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A; Residues: 1-261 <KUR>
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A;Experimental source: strain PCC 7120
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Pred. No. 2.1;
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Wehla
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probable membrane protein YOL003c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein 02389; hypothetical protein UNE3
C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 19-Apr-2
C;Accession: S61981; S66684; S66685; S72130
R;Sterky, F.; Uhlen, M.
Submitted to the EMBL Data Library, December 1995
A;Reference number: S61981
A;Accession: S61981
A;Accession: S61981
A;Accession: S61981
A;Cross-references: EMBL:043491; NID:g1150992; PID:g1150993
R;Petterson, B; Sterky, F.; Uhlen, M.
Submitted to the Protein Sequence Database, July 1996
A;Reference number: S66684
A;Reference number: S66682
A;Accession: S66684
A;Reference number: S66682
A;Accession: S66684
A;Residues: 1-378 <PET>
A;Cross-references: EMBL:274745; NID:g1419764; PID:e251831; PID:g1419765
A;Accession: S66685
A;Accession: S66885

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A; Residues: 1-200 <STO>
A; Cross-references: GB:
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A;Title: Complete genome sequence of the alkaliphil
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Matches 36; Conservative 2
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Pred. No. 3.5;
25; Mismatches
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                PID:g1419765;
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                    MIPS:YOL003c
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                RESULT
AD1305
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A; Genome: mitochondrion
A; Genetic code: SGC6
C; Superfamily: hypothetical protein 1 (CYb-COII intergenic region)
C; Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein 1 (CYb-COII intergenic region) - Leishmania tarentolae C;Species: mitochondrion Leishmania tarentolae C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain S288C
R; Sterky, F.; Holmberg, A.; Pettersson, B.; Uhlen, M.
Yeast 12, 1091-1095, 1996
A; Title: The sequence of a 30 kb fragment on the left arm of chromosome A; Reference number: S72130; MUID:97051599; PMID:8896276
                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-443 <SIM>
A; Cross-references: GB:
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A;Title: Comparison of the maxicircle (mitochondrial) genomes A;Reference number: A92643; MUID:87194837; PMID:3032958
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F;10-26/Domain: transmembrane #status predicted <7
F;124-140/Domain: transmembrane #status predicted
F;173-189/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U43491; NID:g1150992; A;Note: the nucleotide sequence was submitted to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-378 <STW>
A; Cross-references: EMB
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Best Local
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Best Local (
                                                                                                                                                        Matches
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207
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                                                                                                                 FIFLLFFPSFTGVLCTLAITIWRLKPSADCGPFRGLPLFIHSIYSWIDTLSTRPGYLWVV 79
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                                                                           FCFLIFDEEWLGILCLFYILLILFK-----
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23.7%; Pred. No. 8.1;
tive 24; Mismatches
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the codon /
                                                                                                                                                                           Score 80;
Pred. No.
                                                                                                                                                      Mismatches
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9.6;
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                                                                                                                                                                                              Length 443
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RESULT 14
AC2538
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An; Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein all7590 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120bg C; Species: Nostoc sp.
A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Accession: AC2538
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C;Superfamily: lipoprotein signal peptidase
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A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AD1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #tex
C; Accession: AD1305
C; Accession: AD1305
R; Glaser, P: Frangeul, L.; Buchrieser, C.; Amend, A.;
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signal peptidase II homolog lsp [imported] - Listeria monocytogenes (strain
C; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C; Accession: AD1305
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                                                                                                                                                                                                                                                                                            A; Gene: all7590
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                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AP003602; IA;Experimental source: strain PCC
                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-217 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: AB1807; A; Accession: AC2538
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A; Residues: 1-154 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 LCTLAI-----TIWRLKPSADCGPFRGLPLFIHSIYSWIDTLSTRPGYLWVVWI-YRN- 84
62 LLSGWLQSRYPKLDLLSHDVGHLW--WTMLGMKGNPHFNVLHILSNILIFGGFILLASAW
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29; Conserv
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27; Conserv
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%; Pred. No. 4.8;
17; Mismatches
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Dussurget, O.; Entian, K.D.; Fsihi, H.
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Voss, H.; Wehland,
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Search completed: November Job time : 52 secs

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hypothetical protein SA0874 [imported] - Staphylococcus aureus (strain N315) C; Species: Staphylococcus aureus C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C; Accession: H89869
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                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-396 < KUR>
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H89869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
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187 KLTNYNTRPVKAQLRQIVDVTKRHLLLFPGIL 218
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                                                                                                      T-----RPGYLWVVW------IYRNLIGSVH---FFFILTLIVLIITYLYW-----
                                     QITEGRKIMIRLLHEQIINEGKDKMFLIEKLI 139
                                                                           SVEEDKRGKOMGYVYFSWLLGLLVGMVFMNLLIKVHPTRFAFMMSLVVLIAWILYYFVDV
                                                                                                                                                       FILAFTS-----LFLVIW------FPASPFVI--IFSAMMLGIAVSPIWVIMLS
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35; Conserv
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Pred. No. 9
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